

STIC Database Tracking Number: 228790

To: PATRICIA DUFFY
Location: REM-3B05 / Mailbox 3C18
Art Unit: 1645
Thursday, June 28, 2007

Case Serial Number: 09/955502

From: HUGH YOUNG
Location: EIC 1600
REM-1D58 / REM-1A64
Phone: (571)272-5722

hugh.young2@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

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Hugh P. Young Ph.D.
ASRC Management Services
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72448

STIC-Biotech/ChemLib

6-1051

228790

From: Duffy, Patricia
Sent: Friday, June 22, 2007 6:24 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Importance: High

IN RE:09/955,502

Please search SEQ ID NO:11.

Please include a commercial and interference database search.

Please PRINT OUT top 25 hits and deliver to examiner.

11-aa 91
1645
Patricia A. Duffy, Ph.D.
Primary Patent Examiner
571-272-0855,
Remsen 3B05,
Mailbox: 3C18

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JUN 25 2007
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Mg

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

P

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:05:06 ; Search time 39 Seconds
(without alignments)
224.506 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	2 A85954	hypothetical prote
2	486	100.0	91	2 A65082	hypothetical prote
3	486	100.0	91	2 F91108	hypothetical prote
4	469	96.5	91	2 AH0879	conserved hypothet
5	402	82.7	90	2 C82320	conserved hypothet
6	396	81.5	90	2 AI0116	hypothetical prote
7	387	79.6	90	2 C64013	hypothetical prote
8	265	54.5	93	2 E84994	conserved hypothet
9	231	47.5	90	2 H83003	conserved hypothet
10	226	46.5	105	2 C82624	conserved hypothet
11	213	43.8	88	2 H81014	conserved hypothet
12	78	16.0	507	2 C81063	fumarate hydratase
13	78	16.0	546	2 A81807	fumarate hydratase
14	76	15.6	548	2 A54510	63K antigen - nema
15	75.5	15.5	1638	2 D87749	protein unc-73b [i
16	75.5	15.5	2488	2 T42739	guanine nucleotide
17	74.5	15.3	683	2 AC2256	hypothetical prote
18	72	14.8	265	2 T46013	hypothetical prote
19	72	14.8	447	2 T16527	hypothetical prote
20	72	14.8	507	2 A83105	probable fumarase
21	72	14.8	511	2 A99574	ABC transporter at
22	69	14.2	258	2 A97991	hypothetical prote
23	69	14.2	258	2 E95121	phosphoesterase, p
24	69	14.2	548	2 A28209	60K filarial antig
25	69	14.2	1119	2 T15842	hypothetical prote
26	68	14.0	2672	2 A48126	translation activa
27	67.5	13.9	209	2 I64172	hypothetical prote
28	67	13.8	235	2 G65212	hypothetical prote
29	67	13.8	324	2 T05429	hypothetical prote

30	67	13.8	433	2 A70465	probable GTP bindi
31	67	13.8	447	2 JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2 T40058	probable chromatin
33	66.5	13.7	1260	2 T04440	hypothetical prote
34	66	13.6	593	2 C64097	probable soluble 1
35	66	13.6	689	2 F83902	beta-galactosidase
36	65.5	13.5	173	2 H86869	hypothetical prote
37	65.5	13.5	305	2 A75211	asparaginase (EC 3
38	65.5	13.5	323	2 A90536	lipoprotein [impor
39	65.5	13.5	365	2 B54128	Fc-binding protein
40	65.5	13.5	821	2 AI2417	hypothetical prote
41	65	13.4	251	2 E90428	hypothetical prote
42	65	13.4	330	2 S74456	regulatory protein
43	65	13.4	445	1 XUHUMB	alpha-1,3-mannosyl
44	65	13.4	456	2 G71152	hypothetical prote
45	65	13.4	1008	2 H85055	probable transposo
46	65	13.4	1141	2 T29185	hypothetical prote
47	65	13.4	1230	2 S56850	SMC1 protein homol
48	64.5	13.3	245	2 AG2300	hypothetical prote
49	64.5	13.3	305	2 A71247	probable L-asparag
50	64.5	13.3	495	2 AH0985	probable zinc-prot
51	64.5	13.3	859	2 T29630	hypothetical prote
52	64	13.2	220	2 S62410	hypothetical prote
53	64	13.2	438	2 T37786	probable RNA-bindi
54	64	13.2	447	1 A38561	alpha-1,3-mannosyl
55	64	13.2	583	2 T48365	hypothetical prote
56	64	13.2	604	2 S66993	hypothetical prote
57	64	13.2	990	2 T43445	hypothetical prote
58	64	13.2	1051	2 S27002	phospholipase C (E
59	64	13.2	1234	2 S52099	phospholipase C be
60	64	13.2	1234	2 I38994	phospholipase C be
61	63.5	13.1	91	2 H90521	hypothetical prote
62	63.5	13.1	243	2 T29635	hypothetical prote
63	63.5	13.1	460	2 T00639	hypothetical prote
64	63.5	13.1	591	1 FOMVMM	hypothetical prote
65	63	13.0	880	2 AE0179	gag polyprotein -
66	63	13.0	1251	2 A56677	probable ATPase ch
67	63	13.0	1327	2 T14594	neuronal cell cycl
68	63	13.0	1611	1 WMTNPT	guanine nucleoti
69	62.5	12.9	483	1 SYBSET	183K protein - pep
70	62.5	12.9	551	2 E84106	glutamate-tRNA lig
71	62.5	12.9	555	2 C96667	hypothetical prote
72	62.5	12.9	617	2 B71071	unknown protein, 7
73	62.5	12.9	964	1 T04325	probable prolyl en
74	62.5	12.9	1417	2 T00661	probable ATP-depen
75	62	12.8	169	2 PN0560	hypothetical prote
					phytochrome - long

ALIGNMENTS

RESULT 1

A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yggX
C;Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 486; DB 2; Length 91;

Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPPAK 90
 |||||
 RESULT 6
 AI0116
 conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AI0116
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AI0116
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-90 <KUR>
 A:Cross-references: UNIPARC:UPI00000DCCCC4; GB:AL590842; PIDN:CAC89796.1; PID:gl5979022;
 C:Genetics:
 A:Gene: YPO0953
 C:Superfamily: fe(II) trafficking protein YggX
 Query Match 81.5%; Score 396; DB 2; Length 90;
 Best Local Similarity 82.2%; Pred. No. 1.4e-32;
 Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKOTMLINEKKLNMNA 60
 Db 1 MSRTIFCTFLKDAERQDFQLYPGELGKRIYNEISKEAWSQWITKOTMLINEKKLSMMNI 60
 QY 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDK 90
 |||||
 Db 61 EDRKLEQEMVNFLEFGQDVHIAGYTPPSK 90
 |||||
 RESULT 7
 C64013
 hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
 C:Accession: C64013
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
 , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: C64013
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-90 <TIGR>
 A:Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:gl5
 C:Superfamily: fe(II) trafficking protein YggX
 Query Match 79.6%; Score 387; DB 2; Length 90;
 Best Local Similarity 78.2%; Pred. No. 1.1e-31;
 Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKOTMLINEKKLNMNA 60
 Db 1 MARTVFCYLYLKEAEGLDQLYPGELGKRIYNEISKEAWSQWITKOTMLVNEKKLNMNA 60
 QY 61 EHRKLEQEMVNFLEFGKEVHIEGYTP 87
 |||||
 Db 61 EHRKLEQEMVNFLEFGQDVHIAGYTP 87
 |||||
 RESULT 8
 E84994

hypothetical protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: E84994
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84994
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <STO>
A:Cross-references: UNIPARC:UIP000005E610; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yggX; BU553
C:Superfamily: fe(II) trafficking protein YggX

Query Match 54.5%; Score 265; DB 2; Length 93;
Best Local Similarity 61.8%; Pred. No. 1.6e-19;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNISKEAWAQWQHQTMLINEKKLNMMNA 60
| : | | | | | : : : | | | | | : : : | | | : | | | : | | |
Db 17 MNRIIFTFFKKSEGDFFQSYPGKLGGKIYDQISKKAWEKWIEKQTILINEENLNMFN 76

QY 61 EHRKLLQEEMVNFLE 76
| | | : | : | : | :
Db 77 EHRKKIEKYMKLFLEFK 92

RESULT 9
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83003
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UIP000000C5F26; GB:AE004927; GB:AE004091; NID:g9951437; PIDN:
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5148
C:Superfamily: fe(II) trafficking protein YggX

Query Match 47.5%; Score 231; DB 2; Length 90;
Best Local Similarity 51.7%; Pred. No. 3.7e-16;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNISKEAWAQWQHQTMLINEKKLNMMNA 60
| | | : | | | | | : | | | : | | | : | | | : | | | : | | |
Db 1 MSRTVMCRKYHEELPLDRPPYPGAKGEDIYNNVSRAWDWKHWKHQTMLINERRLNMMNA 60

QY 61 EHRKLLQEEMVNFLEPGKVHIEGYTP 87
| | | : | | | | : | | : | | | : | | | : | | |
Db 61 EDRKFLOQMDKFLSGEDYAKADGYVP 87

RESULT 10
C82624
conserved hypothetical protein XF1908 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82624
R:anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Qy	17	QDFQLYPG-ELGKRIYNEISKEAWAQHQTMLINEKTLNNMNAEHRKLLLEQEMVNFLF	75
Db	86	QDSSLYENISVYKNIYLSI-KNSWS-WKIKELSIFFEKYISDYVVKKKIL--NLLNEII	141
Qy	76	EGKEVHIEGYTPEDKK	91
Db	142	EKREI-IOSLNKKOOK	156

RESULT 22
A97991
hypothetical protein spr0953 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A97991
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; E
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A97991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q97QZ0; UNIPROT:Q8CYT2; UNIPARC:UPI0000004A8FC; GB:AE007317;
C:Genetics:
A:Gene: spr0953

Query Match 14.2%; Score 69; DB 2; Length 258;
Best Local Similarity 28.1%; Pred. NO. 16;
Matches 18; Conservative 15; Mismatches 23; Indels 8; Gaps 3;

Qy	28	KRIYNEI--SKEAWAQWQ----	HKQTMLINEKKL--NMNNAEHRKLLQEOMVNELFEGKE	79
		: :	: :	
		: :	: :	
Dd	9	KSVYQELTSKEKFSGFKHTLIHLHTPVSYDYKLFSNWTATKYRKITEDELYDIFFNKK	68	
		:	:	
Qy	80	VHIE	83	
		:	:	
Dd	69	IKVD	72	

RESULT 23
E95121
phosphoesterase, probable [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95121
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A>Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95121
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q97QZ0; UNIPROT:Q8CYT2; UNIPARC:UPI000004A8FC; GB:AE005672;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1052

Query Match	14.2%;	Score 69;	DB 2;	Length 258;
Best Local Similarity	28.1%;	Pred. No. 16;		
Matches 18;	Conservative	15;	Mismatches 23;	Indels 8;
				Gaps 3;

QY 28 KRIYNEI--SKEAWAQWQ----HKQTMLINEKKL--NMNNAEHRKLLQEVMVNFLEGGKE 79
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 9 KSVYOELNSKEKFGSFHKTLLHLHTPVSVDYKLFSNWTATCKRKITEDELYDIFENKK 68

Qy 80 VHI 83
Db 69 IKVD 72

RESULT 24
A28209
60K filarial antigen - nematode (Brugia malayi)
C:Species: Brugia malayi
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: A28209
R:Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Perrine, K.G.; Denker, J.A.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3604-3607, 1988
A>Title: Cloning and characterization of a potentially protective antigen i
A:Reference number: A28209; MUID:88217950; PMID:3368467
A:Accession: A28209
A:Molecule type: mRNA
A:Residues: 1-548 <N1>
A:Cross-references: UNIPROT:P10723; UNIPARC:UPI000016B881; EMBL:J03266; NID
C:Superfamily: lysine-tRNA ligase

Query Match	14.2%;	Score 69;	DB 2;	Length 548;
Best Local Similarity	28.4%;	Pred. No. 38;		
Matches 25;	Conservative	18;	Mismatches 31;	Indels 14;
				Gaps 4;

QY	3	RTIFCTFLQREAGDQFLYPGELGKRIYNEISKEAWAQ-W-QHKQTMLINEKKLMMNA	60
		: : : : : : : :	
D6	23	RTLYOAMIIITKSSKGDFLIRTKDGGQVWEAAASKTALKKSWKRYEQEMLKNEKVA	77

QY 61 EHRKLEQEMWNF-----LFEGKEVHIE 83
| : | : | : |
Db 78 --AKYLEKDTEGVKAALFEAKVOIE 103

RESULT 25
T15842
hypothetical protein C54G7.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15842

A:Submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of *C. elegans* cosmid C54G7.
 A:Reference number: Z18416
 A:Accession: T15842
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1119 <DUZ>
 A:Cross-references: UNIPROT:Q18859; UNIPARC:UPI0000179E
 C:Genetics:
 A:Gene: CESP:C54G7.4
 A:Introns: 6/3; 70/1; 111/2; 160/3; 180/1; 277/1; 325/3

Query Match	14.2%;	Score 69;	DB 2;	Length 1119;
Best Local Similarity	28.7%;	Pred. No. 86;		
Matches 29;	Conservative	16;	Mismatches	38;
			Indels	18;
			Gaps	7;

QY	7	CTFLQ----	REAEGDQFL----	YPGELGKRIYNEISKEAW-AQW-QHKQTMLINEKLN	56
		:	:	:	
		:	:	:	
		:	:	:	
Db	565	CTFTRLAVIKLVEQVPFQFLLYEFDGDELKLIYTSDKRDVWDYEWQDNNMLALKDKQK	6244		
		:	:	:	
		:	:	:	
		:	:	:	
QY	57	MMNAEHRKLLQEEMVN----	FLPEG--KEVHIEG--YTPED	89	
		:::	:::	:::	
		:	:	:	
Db	625	ILICDGSILEOSSVSGSILLFQNLVVTAVNIEKILLTPEN	665		
		:	:	:	
		:	:	:	
		:	:	:	

Search completed: June 27, 2007, 11:11:27
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: June 27, 2007, 10:57:23 ; Search time 215 Seconds
(without alignments)
207.113 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAEQDFQ.....NFLFEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	486	100.0	91	5	ABB78158 Amino aci
2	486	100.0	91	5	ABB78157 Amino aci
3	486	100.0	91	5	ABB78156 Amino aci
4	469	96.5	91	5	ABB78161 Amino aci
5	469	96.5	91	5	ABB78159 Amino aci
6	469	96.5	91	5	ABB78162 Amino aci
7	455	93.6	91	5	ABB78163 Amino aci
8	453	93.2	88	5	ABB78160 Amino aci
9	450	92.6	107	7	ABO65445 Klebsiell
10	436	89.7	126	10	AEB63450 Enterobac
11	402	82.7	90	5	ABB78155 Amino aci
12	396	81.5	90	5	ABB78165 Amino aci
13	395	81.3	78	5	ABB78164 Amino aci
14	389	80.0	93	7	ADF05158 Bacterial
15	388	79.8	91	5	ABB78150 Amino aci
16	387	79.6	87	5	ABB78152 Amino aci
17	379	78.0	87	5	ABB78151 Amino aci
18	373	76.7	87	5	ABB78153 Amino aci
19	332	68.3	88	5	ABB78154 Amino aci
20	265	54.5	76	5	ABB78166 Amino aci
21	255	52.5	87	5	ABB78148 Amino aci
22	255	52.5	87	5	ABB78147 Amino aci

ALIGNMENTS

RESULT 1
ABB78158

ID ABB78158 standard; protein; 91 AA.

XX ABB78158;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

XX

23	241	49.6	86	5	ABB78149	Abb78149 Amino aci
24	231.5	47.6	89	9	AEB41576	Aeb41576 L. pneumo
25	231.5	47.6	95	9	AEB38294	Aeb38294 L. pneumo
26	231	47.5	87	5	ABB78170	Abb78170 Amino aci
27	231	47.5	122	7	ABO74609	AbO74609 Pseudomon
28	227	46.7	88	5	ABB78178	Abb78178 Amino aci
29	227	46.7	90	5	ABB78168	Abb78168 Amino aci
30	225	46.3	87	5	ABB78169	Abb78169 Amino aci
31	216.5	44.5	90	5	ABB78167	Abb78167 Amino aci
32	213	43.8	88	5	ABB78171	Abb78171 Amino aci
33	213	43.8	88	5	ABB78172	Abb78172 Amino aci
34	213	43.8	88	5	ABB78173	Abb78173 Amino aci
35	213	43.8	88	6	ABP77219	Abp77219 N. gonorr
36	206	42.4	87	5	ABB78175	Abb78175 Amino aci
37	200	41.2	87	5	ABB78177	Abb78177 Amino aci
38	200	41.2	87	5	ABB78174	Abb78174 Amino aci
39	200	41.2	87	5	ABB78176	Abb78176 Amino aci
40	199.5	41.0	92	6	ADA34169	Ada34169 Acinetoba
41	131	27.0	110	8	ADL05173	Adl05173 M. catarr
42	83	17.1	506	3	AAy74371	Aay74371 Neisseria
43	83	17.1	1647	4	ABG10750	Abg10750 Novel hum
44	81	16.7	507	6	ABU40210	Abu40210 Protein e
45	78	16.0	507	3	AAy74372	Aay74372 Neisseria
46	78	16.0	507	3	AAy74373	Aay74373 Neisseria
47	78	16.0	546	6	ABU38097	Abu38097 protein e
48	76	15.6	548	4	AAE04737	Aae04737 Brugia ma
49	75	15.4	309	8	ADN46828	Adn46828 Thermococ
50	74.5	15.3	632	8	ADS29711	Ads29711 Bacterial
51	72	14.8	474	7	ABO75727	AbO75727 Pseudomon
52	71.5	14.7	102	9	AED66451	Aed66451 Partial r
53	71.5	14.7	222	9	AED66453	Aed66453 Partial r
54	71.5	14.7	679	9	ADZ85056	Adz85056 Partial F
55	71.5	14.7	1208	9	AED66445	Aed66445 Full-leng
56	71	14.6	311	7	ADM26256	Adm26256 Hyperther
57	70.5	14.5	285	4	AAB92683	Aab92683 Human pro
58	70.5	14.5	414	6	ABU11747	Abu11747 Human MDD
59	70.5	14.5	614	9	ADX06837	Adx06837 Cyclin-de
60	70.5	14.5	614	9	ADY16108	Ady16108 PRO polyp
61	70.5	14.5	764	5	ABB77432	Abb77432 Human tum
62	70.5	14.5	764	7	ADC99062	Adc99062 Human KPP
63	70.5	14.5	817	4	AAm38657	Aam38657 Human pol
64	70.5	14.5	863	4	AAm38656	Aam38656 Human pol
65	70.5	14.5	1135	8	ADS10706	Ads10706 Human the
66	70.5	14.5	1181	8	ADS10708	Ads10708 Human the
67	70.5	14.5	1186	8	ADS10709	Ads10709 Human the
68	70.5	14.5	1188	8	ADH45460	Adh45460 Human mol
69	70.5	14.5	1206	5	ADH48860	Adh48860 NOV61 pro
70	70.5	14.5	1206	5	AEG61819	Aej61819 Human NOV
71	70.5	14.5	1214	7	ADK65785	Adk65785 Angiogene
72	69.5	14.3	374	4	AAm39682	Aam39682 Human pol
73	69.5	14.3	389	4	AAm41468	Aam41468 Human pol
74	69.5	14.3	481	5	AAU93169	Aau93169 Arabidops
75	69.5	14.3	481	7	ADD30148	Add30148 Plant yie

PN US2002072118-A1.
XX 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
PF XX 22-SEP-2000; 2000US-0234588P.
PR XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
PI WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
PS The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX ABB78157;
AC ABB78157;
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA The specification describes a method for reducing superoxide damage to a
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CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX ABB78157;
AC ABB78157;
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
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CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.
XX ABB78156;
AC ABB78156;
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Escherichia coli.
OS US2002072118-A1.
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
PS The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91

PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
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PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
PS The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.
XX ABB78156;
AC ABB78156;
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Escherichia coli.
OS US2002072118-A1.
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
PS The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 91 AA;
Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
QY 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLLQEOMVNFLEFEGKEVHIEGYTPEDKK 91

CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.5e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNA 60
Db 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNA 60
QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 4
ABB78161
ID ABB78161 standard; protein; 91 AA.
XX
AC ABB78161;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
XX US2002072118-A1.
XX 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNA 60
Db 1 MSRTIFCTYLQRDAGEQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNA 60
QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLLLEQEMVNFLEFGKDVHIEGYTPEDKK 91

RESULT 5
ABB78159
ID ABB78159 standard; protein; 91 AA.
XX
AC ABB78159;
XX

DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
XX US2002072118-A1.
XX 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNA 60
Db 1 MSRTIFCTYLQRDAGEQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNA 60
QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91

XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 6
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Salmonella typhi.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 96.5%; Score 469; DB 5; Length 91;
Best Local Similarity 94.5%; Pred. No. 3.2e-46;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLOREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSRTIFCTYLQDAEQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 7
ABB78163
ID ABB78163 standard; protein; 91 AA.
XX
AC ABB78163;
XX
DT 05-NOV-2002 (first entry)
XX

DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Salmonella typhimurium.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 93.6%; Score 455; DB 5; Length 91;
Best Local Similarity 92.3%; Pred. No. 1.4e-44;
Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLOREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSRTIFCTYLQDAEQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 8
ABB78160
ID ABB78160 standard; protein; 88 AA.
XX
AC ABB78160;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX

PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 88 AA;

Query Match 93.2%; Score 453; DB 5; Length 88;
Best Local Similarity 94.3%; Pred. No. 2.2e-44;
Matches 83; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNNA 60
DB 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWHKQTMLINEKKLNMNNA 60

QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPE 88
DB 61 EHRKLLLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 9
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
XX 26-AUG-2003.
PD
XX 27-JAN-2000; 2000US-00489039.
PF
XX 29-JAN-1999; 99US-0117747P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Breton GL, Osborne M;
PI
XX WPI; 2003-895346/82.
XX
DR N-PSDB; ACH98996.
XX

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 107 AA;

Query Match 92.6%; Score 450; DB 7; Length 107;
Best Local Similarity 91.2%; Pred. No. 6.3e-44;
Matches 83; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNNA 60
DB 17 MSRTIFCTFLQREADGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLMMNP 76

QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTPEDKK 91
DB 77 EHRKLLLEQEMVQFLFEGKDVHIEGYTPPEKQ 107

RESULT 10
AEH63450
ID AEH63450 standard; protein; 126 AA.
XX
AC AEH63450;
XX
DT 13-JUL-2006 (first entry)
XX
DE Enterobacter cloacae protein amino acid sequence - SEQ ID 9887.
XX
KW diagnosis; vaccine; bacterial infection; enterobacter infection;
KW antibacterial; screening.
XX
OS Enterobacter cloacae.
XX
PN US7041814-B1.
XX
PD 09-MAY-2006.
XX
PF 18-FEB-1999; 99US-00252691.
XX
PR 18-FEB-1998; 98US-0074787P.
PR 24-JUL-1998; 98US-0094145P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Weinstock KG, Deloughery C, Bush D;
XX
DR WPI; 2006-349670/36.
DR N-PSDB; AEH56055.
XX
PT New nucleic acid encoding an Enterobacter cloacae polypeptide, useful for
PT detecting, preventing, and treating pathological conditions resulting
PT from bacterial infections.
XX
PS Disclosure; SEQ ID NO 9887; 165pp; English.
XX
CC The invention comprises the amino acid and coding sequences of
CC Enterobacter cloacae proteins. The DNA and protein sequences of the
CC invention are useful for detecting, preventing, and treating pathological
CC conditions resulting from bacterial infections, and as components of
CC antibacterial vaccines. The DNA and protein sequences of the invention
CC are also useful in screening for compounds which interfere with the
CC Enterobacter cloacae life cycle or inhibit infection. The present amino
CC acid sequence represents an Enterobacter cloacae protein of the

XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
XX
DE
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Klebsiella pneumoniae.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 78 AA;

Query Match 81.3%; Score 395; DB 5; Length 78;
Best Local Similarity 94.9%; Pred. No. 1e-37;
Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLMMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLMMNP 60

QY 61 EHRKLEQEMVNFLEFGK 78
Db 61 EHRKLEQEMVQFLFEGK 78

RESULT 14
ADF05158
ID ADF05158 standard; protein; 93 AA.
XX
AC ADF05158;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polypeptide #1271.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
OS Proteus mirabilis.
XX
PN US6605709-B1.

XX 12-AUG-2003.
PD
XX
PF 05-APR-2000; 2000US-00543681.
XX
PR 09-APR-1999; 99US-0128706P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL;
XX
DR WPI; 2003-895291/82.
DR N-PSDB; ADF00986.
XX
PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
PS Disclosure; SEQ ID NO 5443; 870pp; English.
XX
CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 93 AA;

Query Match 80.0%; Score 389; DB 7; Length 93;
Best Local Similarity 80.0%; Pred. No. 6.1e-37;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLMMNA 60
Db 4 MSRTIFCTFLNKEADGLDFQLYPGELGKRIYNEISKEAWGQWMAKQTMLINEKKLNTMNP 63

QY 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDK 90
Db 64 DDRKLEQEMVRFLEGHVDHIDGYTPPEK 93

RESULT 15
ABB78150
ID ABB78150 standard; protein; 91 AA.
XX
AC ABB78150;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.


```

XX SQ Sequence 87 AA;
Query Match 78.0%; Score 379; DB 5; Length 87;
Best Local Similarity 75.9%; Pred. No. 8.1e-36;
Matches 66; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGDFFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60
Db 1 MARTVFCEYLKQESEGLDFQLYPGELGKRIFDSISKQAWREWKKQTMLVNEKLNMMNA 60
QY 61 EHRKLLEQEMVNFLFEGKDVHIEGYTP 87
Db 61 DHRQLLEQEMVNFLFEGKDVHIEGYVP 87

RESULT 18
ID ABB78153 standard; protein; 87 AA.
XX ABB78153;
AC XX
DT 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
KW Unidentified.
OS US2002072118-A1.
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-009555502.
XX 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
PI WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
PS Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX Sequence 87 AA;

Query Match 76.7%; Score 373; DB 5; Length 87;
Best Local Similarity 75.9%; Pred. No. 4e-35;
Matches 66; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGDFFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60
Db 1 MARVMFCEYLKKEAEGLDFQLYPGELGKRIFNSISKQAWAEWIKKQTMLVNEKLNMMNP 60

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DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 76 AA;
XX
Query Match 54.5%; Score 265; DB 5; Length 76;
Best Local Similarity 61.8%; Pred. No. 1.le-22;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKNMNA 60
Db 1 MNRIFCTFFKKKSEGQDFQSPGKLGKKIYDQISKKAWEKWIEKQTILINEENLNMFL 60
QY 61 EHRKLLQEMVNFLE 76
Db 61 EHRKKIEKYMKCLFLFK 76
RESULT 21
ABB78148
ID ABB78148 standard; protein; 87 AA.
XX
AC ABB78148;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS -Bordetella parapertussis.
XX
PN US2002072118-A1.
XX
```

```
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;
XX
Query Match 52.5%; Score 255; DB 5; Length 87;
Best Local Similarity 55.2%; Pred. No. 1.9e-21;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKNMNA 60
Db 1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIWQQISKEAWEWKQIQTRLVNNENRLNLADA 60
QY 61 EHRKLLQEMVNFLEFEGKEVHIEGYP 87
Db 61 RARKYLOQQMERFLFEDGTVEAQQGYVP 87
RESULT 22
ABB78147
ID ABB78147 standard; protein; 87 AA.
XX
AC ABB78147;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella pertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
```


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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:01:26 ; Search time 347 Seconds
(without alignments)
281.162 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 8.4.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	486	100.0	91	1	FETP SHIBS	Q31wm4 shigella bo
2	486	100.0	91	1	FETP SHIDS	Q32c31 shigella dy
3	486	100.0	91	1	FETP SHISS	Q3yxe9 shigella so
4	486	100.0	91	2	Q1R763_ECOUT	Q1r763 escherichia
5	481	99.0	90	1	FETP_ECO57	P0a8p4 escherichia
6	481	99.0	90	1	FETP_ECOLI	P0a8p3 escherichia
7	481	99.0	90	1	FETP_SHIFL	P0a8p5 shigella fl
8	477	98.1	90	1	FETP_ECOL6	Q8fe19 escherichia
9	464	95.5	90	1	FETP_SALCH	Q57k04 salmonella
10	464	95.5	90	1	FETP_SALPA	Q5pmm1 salmonella
11	464	95.5	90	1	FETP_SALTI	P67618 salmonella
12	464	95.5	90	1	FETP_SALTY	P67617 salmonella
13	411	84.6	90	1	FETP_ERWCT	Q6d8j9 erwinia car
14	404	83.1	90	1	FETP_YERPS	Q666m3 yersinia ps
15	402	82.7	90	1	FETP_VIBCH	Q9kur4 vibrio chol
16	402	82.7	90	1	FETP_VIBVU	Q8dcc5 vibrio vuln
17	402	82.7	90	1	FETP_VIBVY	Q7mhi4 vibrio vuln
18	399	82.1	90	1	FETP_VIBPA	Q87ll5 vibrio para
19	397	81.7	90	2	Q1V3X2_VIBAL	Q1v3x2 vibrio algi
20	396	81.5	90	1	FETP_YERPE	Q8zhe7 yersinia pe
21	396	81.5	90	2	Q1CEV2_YERPE	Q1cev2 yersinia pe
22	396	81.5	90	2	Q1CB93_YERPE	Q1cb93 yersinia pe
23	390	80.2	90	1	FETP_SODGM	Q2nrb4 sodalis glo
24	389	80.0	91	1	FETP_MANSM	Q65vt7 mannheimia
25	387	79.6	90	1	FETP_HAEI8	Q4qmd9 haemophilus
26	387	79.6	90	1	FETP_HAEIN	P44048 haemophilus
27	382	78.6	90	1	FETP_PHOPR	Q6lmk7 photobacter
28	382	78.6	90	2	Q1Z4G3_PHOPR	Q1z4g3 photobacter
29	381	78.4	90	1	FETP_PHOLL	Q7n7i1 photorhabdu
30	379	78.0	90	1	FETP_PASMU	Q9clb9 pasteurella
31	374	77.0	90	2	Q1ZNG9_9VIBR	Q1zng9 vibrio angu

32	373	76.7	94	1	FETP_HAEDU	Q7vkb6 haemophilus
33	371	76.3	90	2	Q2C3L2_9GAMM	Q2c3l2 photobacter
34	366	75.3	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
35	363	74.7	90	1	FETP_PSEHT	Q3ili9 pseudoalter
36	351	72.2	91	2	Q3QJD7_9GAMM	Q3qjd7 shewanella
37	343	70.6	92	2	Q33Q73_9GAMM	Q33q73 shewanella
38	342	70.4	92	2	Q2ZRK9_SHEPU	Q2zrk9 shewanella
39	342	70.4	92	2	Q3Q7K0_9GAMM	Q3q7k0 shewanella
40	340	70.0	91	2	Q3P4C9_9GAMM	Q3p4c9 shewanella
41	339	69.8	92	2	Q2X4M4_9GAMM	Q2x4m4 shewanella
42	338	69.5	92	2	Q2Z5M5_9GAMM	Q2z5m5 shewanella
43	338	69.5	92	2	Q368P1_9GAMM	Q368p1 shewanella
44	335	68.9	90	1	FETP_IDILO	Q5qy58 idiomarina
45	335	68.9	92	2	Q3NME3_SHEFR	Q3nme3 shewanella
46	332	68.3	92	1	FETP_SHEON	Q8ebx6 shewanella
47	326	67.1	89	2	Q1FVU6_9GAMM	Q1fvu6 psychromona
48	324	66.7	90	1	FETP_COLP3	Q47wl9 colwellia p
49	318	65.4	90	2	Q15ZT1_ALTAT	Q15zt1 pseudoalter
50	316	65.0	89	2	Q1ZE27_9GAMM	Q1zf27 psychromona
51	283	58.2	77	2	Q1LSZ8_BAUCH	Q1lsz8 baumannia c
52	265	54.5	77	1	FETP_BUCAI	P57618 buchnera ap
53	255	52.5	90	1	FETP_BORAI	Q2kyq6 bordetella
54	255	52.5	90	1	FETP_BORBR	Q7wh06 bordetella
55	255	52.5	90	1	FETP_BORPA	Q7w9q2 bordetella
56	255	52.5	90	1	FETP_BORPE	Q7vwc4 bordetella
57	247	50.8	78	1	FETP_BUCAP	Q8k925 buchnera ap
58	239	49.2	90	1	FETP_NITOC	Q3j8x0 nitrosococc
59	237.5	48.9	84	1	FETP_BLOPB	Q493f6 blochmannia
60	237	48.8	90	1	FETP_DECAR	Q47a19 dechloromon
61	235	48.4	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
62	233	47.9	90	1	FETP_RHOFD	Q21wm7 rhodofera
63	231.5	47.6	89	1	FETP_LEGPA	Q5x3x9 legionella
64	231.5	47.6	89	1	FETP_LEGPH	Q5zu80 legionella
65	231	47.5	90	1	FETP_PSEAE	Q9hu36 pseudomonas
66	231	47.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
67	230	47.3	109	2	Q1H533_METFL	Q1h533 methylobaci
68	229	47.1	91	1	FETP_XANC5	Q3brx9 xanthomonas
69	228.5	47.0	89	1	FETP_LEGPL	Q5wvc4 legionella
70	227	46.7	90	1	FETP_COXBU	Q83d06 coxiella bu
71	227	46.7	90	1	FETP_PSE14	Q48c72 pseudomonas
72	227	46.7	90	1	FETP_PSESM	Q87uf5 pseudomonas
73	227	46.7	90	1	FETP_PSEU2	Q4zlp3 pseudomonas
74	226	46.5	90	1	FETP_XYLFA	Q9pc73 xylella fas
75	225	46.3	90	1	FETP_PSEPK	Q88r49 pseudomonas

ALIGNMENTS

RESULT 1
FETP_SHIBS
ID FETP_SHIBS STANDARD; PRT; 91 AA.
AC Q31WM4;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2005, sequence version 1.
DT 11-JUL-2006, entry version 7.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=SBO_3028;
OS Shigella boydii serotype 4 (strain Sb227).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300268;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron

CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
DR EMBL: CP000036; ABB67534.1; -; Genomic_DNA.
DR SMR; Q31WM4; 1-91.
DR GenomeReviews; CP000036_GR; SBO_3028.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000246116.
SQ SEQUENCE 91 AA; 10953 MW; 1E3625B77C32B94B CRC64;

Query Match 100.0%; Score 486; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.3e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

RESULT 2
FETP_SHIDS
ID FETP_SHIDS STANDARD; PRT; 91 AA.
AC Q32C31;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2005, sequence version 1.
DT 11-JUL-2006, entry version 7.
DE Probable Fe(2+)-trafficking protein.
GN Name=YggX; OrderedLocusNames=SDY_3110;
OS Shigella dysenteriae serotype 1 (strain Sd197).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery.";
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL: CP000034; ABB63124.1; -; Genomic_DNA.
DR SMR; Q32C31; 1-91.
DR GenomeReviews; CP000034_GR; SDY_3110.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.

DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000246117.
SQ SEQUENCE 91 AA; 10953 MW; 1E3625B77C32B94B CRC64;

Query Match 100.0%; Score 486; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.3e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

RESULT 3
FETP_SHISS
ID FETP_SHISS STANDARD; PRT; 91 AA.
AC Q3YXE9;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 27-SEP-2005, sequence version 1.
DT 11-JUL-2006, entry version 9.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=SSO_3234;
OS Shigella sonnei (strain Ss046).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300269;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery.";
RL Nucleic Acids Res. 33:6445-6458(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL: CP000038; AAZ89813.1; -; Genomic_DNA.
DR SMR; Q3YXE9; 1-91.
DR GenomeReviews; CP000038_GR; SSO_3234.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000246118.
SQ SEQUENCE 91 AA; 10953 MW; 1E3625B77C32B94B CRC64;

Query Match 100.0%; Score 486; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.3e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||||
RESULT 4
Q1R763 ECOUT PRELIMINARY; PRT; 91 AA.
AC Q1R763;
DT 16-MAY-2006, integrated into UniProtKB/TrEMBL.
DT 16-MAY-2006, sequence version 1.
DT 11-JUL-2006, entry version 4.
DE Hypothetical protein yggX.
GN Name=yggX; ORFNames=UT189_C3353;
OS Escherichia coli (strain UT189 / UPEC).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=364106;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UTI89;
RX PubMed=16585510; DOI=10.1073/pnas.0600938103;
RA Chen S.-L., Hung C.-S., Xu J., Reigstad C.S., Magrini V., Sabo A.,
RA Blasiar D., Bieri T., Meyer R.R., Ozersky P., Armstrong J.R.,
RA Fulton R.S., Latreille J.P., Spieth J., Hooton T.M., Mardis E.R.,
RA Hultgren S.J., Gordon J.I.;
RT "Identification of genes subject to positive selection in
RT uropathogenic strains of Escherichia coli: A comparative genomics
RT approach.";
RL Proc. Natl. Acad. Sci. U.S.A. 103:5977-5982(2006).
CC -----
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CC -----
DR EMBL; CP000243; ABE08801.1; -; Genomic_DNA.
DR SMR; Q1R763; 1-91.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10953 MW; 1E3625B877C32B94B CRC64;
Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.3e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNA 60
|
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNA 60
|
QY 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|
Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|
RESULT 5
FETP ECO57 STANDARD; PRT; 90 AA.
AC P0A8P4; P52065;
DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 1.
DT 11-JUL-2006, entry version 11.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=Z4307, ECs3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX .MEDLINE=21074935; PubMed=11205551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 050952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL; AE005174; AAG58093.1; -; Genomic_DNA.
DR EMBL; BA000007; BAB37261.1; -; Genomic_DNA.
DR PIR; A85954; A85954.
DR PIR; F91108; F91108.
DR SMR; P0A8P4; 1-90.
DR GenomeReviews; BA000007 GR; ECs3838.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
FT /FTId=PRO_0000214479.
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;
Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNAE 61
|
Db 1 SRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNAE 60
|
QY 62 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 91
|
Db 61 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 90
|
RESULT 6
FETP_ECOLI STANDARD; PRT; 90 AA.
AC P0A8P3; P52065; Q2M9N1;
DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 1.
DT 11-JUL-2006, entry version 12.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655 / ATCC 47076;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;
RX DOI=10.1038/msb4100049;
RA Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,
RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
RT "Highly accurate genome sequences of Escherichia coli K-12 strains
MG1655 and W3110.";
RL Mol. Syst. Biol. 2:E1-E5(2006).
RN [3]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [4]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphery-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12.";
RL FEMS Microbiol. Lett. 169:375-382(1998).
RN [5]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [6]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the yggX gene of
Escherichia coli.";
RL J. Bacteriol. 185:6624-6632(2003).
RN [7]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein YggX
from Escherichia coli.";
RL Protein Sci. 14:1673-1678(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes. Necessary to
maintain high levels of aconitase under oxidative stress.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- INDUCTION: By oxidative stress and soxS.
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
CC -----
DR EMBL: U28377; AA69129.1; -; Genomic DNA.
DR EMBL: U00096; AAC75999.1; -; Genomic DNA.
DR EMBL: AP009048; BAE77025.1; -; Genomic DNA.
DR PIR: A65082; A65082.
DR PDB: 1YHD; NMR; A=1-90.
DR SWISS-2DPAGE; P0A8P3; COLI.
DR GenomeReviews; U00096 GR; b2962.

DR EchoBASE; EB2809; --
DR EcoGene; EG12984; yggX.
DR HAMAP; MF 00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW 3D-structure; Complete proteome; Direct protein sequencing; Iron.
FT INIT MET 0
FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000214478.
FT STRAND 4 5
FT STRAND 7 9
FT STRAND 11 13
FT STRAND 17 18
FT STRAND 21 22
FT TURN 23 24
FT TURN 25 32
FT HELIX 33 33
FT STRAND 35 51
FT TURN 52 53
FT TURN 56 57
FT STRAND 58 58
FT HELIX 59 72
FT TURN 73 77
FT STRAND 88 88
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAEAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61
|||
Db 1 SRTIFCTFLQREAEAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 60

QY 62 HRKLLQEOMVNFLEFGKEVHIEGYTPEDKK 91
|||
Db 61 HRKLLQEOMVNFLEFGKEVHIEGYTPEDKK 90

RESULT 7
FETP SHIFL STANDARD; PRT; 90 AA.
ID POA8P5; PS2065;
DT 07-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 1.
DT 25-JUL-2006, entry version 12.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=SF2959, S_3162;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 700930 / 2457T / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC
CC EMBL; AE005674; AAN44440.1; -; Genomic_DNA.
CC EMBL; AE014073; AAP18264.1; -; Genomic_DNA.
CC SMR; POA8P5; 1-90.
CC GenomeReviews; AE014073 GR; S 3162.
CC GenomeReviews; AE005674 GR; SF2959.
CC HAMAP; MF 00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron traffic; 1.
CC PIRSF; PIRSF029827; Fe traffic_yggX; 1.
CC ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000214507.
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 61
|||||
Db 1 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||||
Db 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90

By similarity.
Probable Fe(2+)-trafficking protein.
/FTid=PRO_0000214507.

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 61
|||||
Db 1 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||||
Db 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90

RESULT 8
FETP_ECOL6
ID_FETP_ECOL6 STANDARD; PRT; 90 AA.
AC Q8FE19;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 25-JUL-2003, sequence version 2.
DT 11-JUL-2006, entry version 21.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=c_3550;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.F., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC

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CC
CC EMBL; AE014075; AAN81998.1; -; Genomic_DNA.
CC SMR; Q8FE19; 1-90.
CC GenomeReviews; AE014075 GR; C 3550.
CC BioCyc; ECOL199310:C3550-MONOMER; -.
CC HAMAP; MF 00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron traffic; 1.
CC PIRSF; PIRSF029827; Fe traffic_yggX; 1.
CC ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000214480.
SQ SEQUENCE 90 AA; 10805 MW; D7C66C2A35E63692 CRC64;

Query Match 98.1%; Score 477; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6e-41;
Matches 89; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 61
|||||
Db 1 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||||
Db 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90

By similarity.
Probable Fe(2+)-trafficking protein.
/FTid=PRO_0000214480.

Query Match 98.1%; Score 477; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6e-41;
Matches 89; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 61
|||||
Db 1 SRTIFCTFLOREAEAGDQFLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNAE 60

QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||||
Db 61 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 90

RESULT 9
FETP_SALCH
ID_FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 2.
DT 11-JUL-2006, entry version 13.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=Sch_3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC
CC EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
CC SMR; Q57K04; 1-90.
CC GenomeReviews; AE017220 GR; SCH_3052.
CC HAMAP; MF 00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron traffic; 1.
CC ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO_0000214502.

SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
Query Match 95.5%; Score 464; DB 1; Length 90;
Best Local Similarity 94.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61
Db 1 SRTIFCTYLQDAEGDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 HRKLEQEMVSFLFEGKDVHIEGYTPEDKK 90
RESULT 10
FETP_SALPA
ID_FETP_SALPA STANDARD; PRT; 90 AA.
AC Q5PMM1;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 2.
DT 11-JUL-2006, entry version 11.
DE Probable Fe(2+)-trafficking protein.
GN Name=YggX; OrderedLocusNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparative genome degradation in Paratyphi A and Typhi, human-
restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC
CC EMBL; CP0000026; AAV78812.1; -; Genomic_DNA.
DR SMR; Q5PMM1; 1-90.
DR GenomeReviews; CP0000026_GR; SPA2974.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
FT CHAIN 1 90
FT By similarity.
FT Probable Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214503.
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
Query Match 95.5%; Score 464; DB 1; Length 90;
Best Local Similarity 94.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61
Db 1 SRTIFCTYLQDAEGDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

Db 61 HRKLEQEMVSFLFEGKDVHIEGYTPEDKK 90
RESULT 11
FETP_SALTI
ID_FETP_SALTI STANDARD; PRT; 90 AA.
AC P67618; Q8XFV6;
DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2004, sequence version 1.
DT 11-JUL-2006, entry version 14.
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocusNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 700931 / Ty2;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC
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CC
CC EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR EMBL; AE014613; AAO70576.1; -; Genomic_DNA.
DR SMR; P67618; 1-90.
DR GenomeReviews; AL513382_GR; STY3266.
DR GenomeReviews; AE014613_GR; t3024.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
FT CHAIN 1 90
FT By similarity.
FT Probable Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214504.
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
Query Match 95.5%; Score 464; DB 1; Length 90;
Best Local Similarity 94.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61

Db 1 SRTIFCTYLORDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60

QY 62 HRKLLQEEMVNFLFEGKEVHIEGYTPEDKK 91

Db 61 HRKLLQEEMVSFLFEGKDVHIEGYTPEDKK 90

RESULT 12

FETP_SALTY

ID FETP_SALTY STANDARD; PRT; 90 AA.

AC P67617; Q8XFFV6;

DT 11-OCT-2004, integrated into UniProtKB/Swiss-Prot.

DT 11-OCT-2004, sequence version 1.

DT 11-JUL-2006, entry version 16.

DE Probable Fe(2+)-trafficking protein.

GN Name=yggX; OrderedLocusNames=STM3111;

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";

RT Nature 413:852-856 (2001).

RL [2]

RN FUNCTION.

RP STRAIN=LT2;

RC PubMed=11416172; DOI=10.1073/pnas.151243198;

RX Gralnick J.A., Downs D.M.;

RA "Protection from superoxide damage associated with an increased level of the YggX protein in Salmonella enterica.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:8030-8035 (2001).

RN [3]

RP FUNCTION, AND MUTAGENESIS OF CYS-6.

RC STRAIN=LT2;

RX PubMed=12670952; DOI=10.1074/jbc.M301577200;

RA Gralnick J.A., Downs D.M.;

RT "The YggX protein of Salmonella enterica is involved in Fe(II) trafficking and minimizes the DNA damage caused by hydroxyl radicals: residue Cys-7 is essential for YggX function.";

RT J. Biol. Chem. 278:20708-20715 (2003).

RN [4]

RP FUNCTION.

RC STRAIN=LT2;

RX PubMed=15516576; DOI=10.1128/JB.186.22.7626-7634.2004;

RA Skovran E., Lauhon C.T., Downs D.M.;

RT "Lack of YggX results in chronic oxidative stress and uncovers subtle defects in Fe-S cluster metabolism in Salmonella enterica.";

RL J. Bacteriol. 186:7626-7634 (2004).

CC -!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes. Necessary to maintain high levels of aconitase under oxidative stress.

CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.

CC

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CC

DR EMBL; AE008843; AAL21986.1; -; Genomic_DNA.

DR PDB; 1XS8; NMR; A=1-90.

DR GenomeReviews; AE006468_GR; STM3111.

DR StyGene; SG????; yggX.

DR HAMAP; MF_00686; -; 1.

DR InterPro; IPR007457; yggX.

DR Pfam; PF04362; Iron_traffic; 1.

DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.

DR ProDom; PD029191; DUF495; 1.

KW 3D-structure; Complete proteome; Iron.

FT INIT_MET 0 By similarity.

FT CHAIN 1 90 Probable Fe(2+)-trafficking protein.

FT /FTid=PRO_0000214505.

FT C->S: Strong decrease in activity.

FT MUTAGEN 6 6

FT STRAND 3 5

FT TURN 7 9

FT STRAND 10 15

FT STRAND 20 21

FT STRAND 23 23

FT HELIX 24 30

FT TURN 31 32

FT STRAND 34 34

FT HELIX 35 52

FT TURN 56 57

FT STRAND 58 58

FT HELIX 59 73

FT TURN 74 74

FT STRAND 78 79

FT STRAND 83 84

FT STRAND 87 88

SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;

Query Match 95.5%; Score 464; DB 1; Length 90;

Best Local Similarity 94.4%; Pred. No. 1.3e-39;

Matches 85; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAEQGDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNAE 61

Db 1 SRTIFCTYLORDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60

QY 62 HRKLLQEEMVNFLFEGKEVHIEGYTPEDKK 91

Db 61 HRKLLQEEMVSFLFEGKDVHIEGYTPEDKK 90

RESULT 13

FETP_ERWCT

ID FETP_ERWCT STANDARD; PRT; 90 AA.

AC Q6D8J9;

DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.

DT 16-AUG-2004, sequence version 1.

DT 11-JUL-2006, entry version 13.

DE Probable Fe(2+)-trafficking protein.

GN OrderedLocusNames=ECA0975;

OS Erwinia carotovora subsp. atroseptica (Pectobacterium atrosepticum).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Pectobacterium.

OX NCBI_TaxID=29471;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=SCRI 1043 / ATCC BAA-672;

RX PubMed=15263089; DOI=10.1073/pnas.0402424101;

RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J., Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K., Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J., Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H., Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S., Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

RT "Genome sequence of the enterobacterial phytopathogen Erwinia carotovora subsp. atroseptica and characterization of virulence factors.";

RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).

CC -!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.

CC

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RESULT 16
FETP_VIBVU
ID_FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DC5;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2003, sequence version 1.
DT 11-JUL-2006, entry version 19.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VV1_1514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE016795; AA009940.1; -; Genomic_DNA.
CC GenomeReviews; AE016795 GR; VV1_1514.
CC BioCyc; VVUL216895:VV11514-MONOMER; -.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron traffic; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
KW CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTId=PRO_0000214511.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 3e-33;
Matches 74; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMDP 60

QY 61 EHRKLLLEQEMVNFLEEGKEVHIEGYTPEDK 90
Db 61 EHRKLLLETEMVNFLEEGKEVHIEGYTPPSK 90

RESULT 17
FETP_VIBVY
ID_FETP_VIBVY STANDARD; PRT; 90 AA.
AC Q7MHI4;
DT 10-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-2003, sequence version 1.
DT 11-JUL-2006, entry version 20.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VV2885;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,

Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 3e-33;
Matches 74; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMDP 60

QY 61 EHRKLLLEQEMVNFLEEGKEVHIEGYTPEDK 90
Db 61 EHRKLLLETEMVNFLEEGKEVHIEGYTPPSK 90

RESULT 18
FETP_VIBPA
ID_FETP_VIBPA STANDARD; PRT; 90 AA.
AC Q87LI5;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 11-JUL-2006, entry version 18.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VP2627;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
CC EMBL; BA000031; BAC60890.1; -; Genomic_DNA.
CC SMR; Q87LI5; 1-87.
CC GenomeReviews; BA000031 GR; VP2627.
CC HAMAP; MF_00686; -; 1.
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RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
CC EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
CC GenomeReviews; BA000037 GR; VV2885.
CC BioCyc; VVUL196600:VV2885-MONOMER; -.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; Iron traffic; 1.
CC PIRSF; PIRSF029827; Fe traffic_YggX; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
KW CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTId=PRO_0000214512.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 82.7%; Score 402; DB 1; Length 90;
Best Local Similarity 82.2%; Pred. No. 3e-33;
Matches 74; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMDP 60

QY 61 EHRKLLLEQEMVNFLEEGKEVHIEGYTPEDK 90
Db 61 EHRKLLLETEMVNFLEEGKEVHIEGYTPPSK 90

RESULT 18
FETP_VIBPA
ID_FETP_VIBPA STANDARD; PRT; 90 AA.
AC Q87LI5;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 11-JUL-2006, entry version 18.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=VP2627;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
CC EMBL; BA000031; BAC60890.1; -; Genomic_DNA.
CC SMR; Q87LI5; 1-87.
CC GenomeReviews; BA000031 GR; VP2627.
CC HAMAP; MF_00686; -; 1.
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DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214510.
SQ SEQUENCE 90 AA; 10629 MW; A20D59535F0F9A1B CRC64;

Query Match 82.1%; Score 399; DB 1; Length 90;
Best Local Similarity 83.9%; Pred. No. 6e-33;
Matches 73; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTVFCARLKKEGGLDFQLYPGELGKRIFDNIKEAWAQWQHKTMLINEKKLNMMNDP 60

QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTP 87
Db 61 EHRKLLLETEMVNFLEFGKDVHIEGYTP 87

RESULT 19
Q1V3X2 VIBAL PRELIMINARY; PRT; 90 AA.
AC Q1V3X2;
DT 16-MAY-2006, integrated into UniProtKB/TrEMBL.
DT 16-MAY-2006, sequence version 1.
DT 11-JUL-2006; entry version 3.
DE Hypothetical protein.
GN ORFNames=V12G01.14084;
OS Vibrio alginolyticus 12G01.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=314288;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12G01;
RA Polz M., Ferrera S., Johnson J., Kravitz S., Halpern A.,
RA Remington K., Beeson K., Tran B., Rogers Y.-H., Friedman R.,
RA Venter J.C.;
RL Submitted (MAR-2006) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAP01000056; EAS74087.1; -; Genomic_DNA.
DR SMR; Q1V3X2; 1-87.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10629 MW; A75D0C535F0F9A1B CRC64;

Query Match 81.7%; Score 397; DB 2; Length 90;
Best Local Similarity 82.8%; Pred. No. 9.7e-33;
Matches 72; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTVFCARLKKEGGLDFQLYPGELGKRIFDNIKEAWAQWQHKTMLINEKKLNMMNDP 60

QY 61 EHRKLLLEQEMVNFLEFGKEVHIEGYTP 87
Db 61 EHRKLLLETEMVNFLEFGKDVHIEGYTP 87

RESULT 20
FETP_YERPE
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ID AC Q8ZHE7;
DT 25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 11-JUL-2006, entry version 30.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=YPO0953, Y3340, YP3488;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titchall R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
DR EMBL; AJ414145; CAC89796.1; -; Genomic_DNA.
DR EMBL; AE009952; AAM86890.1; -; Genomic_DNA.
DR EMBL; AE017140; AAS63643.1; -; Genomic_DNA.
DR SMR; Q8ZHE7; 1-90.
DR GenomeReviews; AE009952 GR; Y3340.
DR GenomeReviews; AE017042 GR; YP3488.
DR GenomeReviews; AL590842 GR; YPO0953.
DR BioCyc; YPES187410:Y3340-MONOMER; -.
DR BioCyc; YPES632:YPO0953-MONOMER; -.
DR HAMAP; MF_00686; -.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron_traffic; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTID=PRO_0000214519.
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11-JUL-2006, integrated into UniProtKB/TrEMBL.
11-JUL-2006, sequence version 1.
11-JUL-2006, entry version 1.
Hypothetical protein.
ORFNames=YPA_0311;
Yersinia pestis Antiqua.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=360102;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=Antiqua;
PubMed=16740952; DOI=10.1128/JB.00124-06;
Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
Vergez L.M., Worsham P., Chu M.C., Andersen G.L.;
"Complete Genome Sequence of Yersinia pestis Strains Antiqua and
Nepal516: Evidence of Gene Reduction in an Emerging Pathogen.";
J. Bacteriol. 188:4453-4463(2006).
[2]
NUCLEOTIDE SEQUENCE.
STRAIN=Antiqua;
US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C.,
Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
Chain P., Hu P., Malfatti S.A., Radnedge L., Vergez L.M., Larimer F.,
Land M., Hauser L., Worsham P., Chu M.C., Andersen G.L.,
Richardson P.;
"Complete sequence of chromosome of Yersinia pestis Antiqua.";
Submitted (APR-2006) to the EMBL/GenBank/DBJ databases.
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EMBL; CP000308; ABG12279.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;

Query Match      81.5%;   Score 396;   DB 2;   Length 90;
Best Local Similarity 82.2%;   Pred. NO. 1.2e-32;
Matches 74;   Conservative 8;   Mismatches 8;   Indels 0;   Gaps

QY      1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA 60
Db      1 MSRTIFCTFLKQDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKKLSMMNI 60

QY      61 EHRKLLQEQMVNLFEGKEVHIEGYTPEDK 90
Db      61 EDRKLLQEQMVNLFEGQDVHIAGYTPPSK 90

RESULT 23
FETP_SODGM
ID_FETP_SODGM      STANDARD;      PRT;      90 AA.
AC_Q2NRB4;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 07-FEB-2006, sequence version 1.
DT 25-JUL-2006, entry version 6.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=SG2036;
OS Sodalis glossinidius (strain morsitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16365377; DOI=10.1101/gr.4106106;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron

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CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
DR EMBL; AP008232; BAE75311.1; -; Genomic_DNA.
DR SMR; Q2NRB4; 1-87.
DR GenomeReviews; AP008232_GR; SG2036.
DR HAMAP; MF 00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO 0000246119.
SQ SEQUENCE 90 AA; 10701 MW; E9016C38A5D05394 CRC64;

Query Match 80.2%; Score 390; DB 1; Length 90;
Best Local Similarity 80.5%; Pred. No. 5.1e-32;
Matches 70; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60
Db 1 MSRTIYCTFLKREAGQDFQYPGELGKRIYDNISKEAWTQWTKQTMLINEKISVMNV 60

QY 61 EHRKLLQEQMVNLFEGKEVHIEGYTP 87
Db 61 ADRKVLQEQEMINFLFEGQDVHIQGYTP 87

RESULT 24
FETP_MANSM
ID FETP_MANSM STANDARD; PRT; 91 AA.
AC Q65VT7;
DT 19-JUL-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2004, sequence version 1.
DT 11-JUL-2006, entry version 12.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=MS0316;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OC NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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CC -----
DR EMBL; AE016827; AAU36923.1; -; Genomic_DNA.
DR SMR; Q65VT7; 1-88.
DR GenomeReviews; AE016827_GR; MS0316.
DR HAMAP; MF 00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 91
FT Probable Fe(2+)-trafficking protein.
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FT SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AACC CRC64;
SQ /FTid=PRO 0000214489.

Query Match 80.0%; Score 389; DB 1; Length 91;
Best Local Similarity 78.4%; Pred. No. 6.5e-32;
Matches 69; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60
Db 1 MSRTVFCGYLKQEAEGDLDFQLYPGELGKRIYDNISKEAWGEWMKKQTMVLVNEKLNMMNA 60

QY 61 EHRKLLQEQMVNLFEGKEVHIEGYTP 88
Db 61 DHRKLLQEQMVNLFEGKDVHIEGYIPQ 88

RESULT 25
FETP_HAEI8
ID FETP_HAEI8 STANDARD; PRT; 90 AA.
AC Q4QMD9;
DT 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
DT 19-JUL-2005, sequence version 1.
DT 11-JUL-2006, entry version 7.
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocusNames=NTHI0920;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=281310;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20."
RL J. Bacteriol. 187:4627-4636(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC -----
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CC -----
DR EMBL; CP000057; AAX87808.1; -; Genomic_DNA.
DR SMR; Q4QMD9; 1-87.
DR GenomeReviews; CP000057_GR; NTHI0920.
DR HAMAP; MF 00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; Iron traffic; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CHAIN 1 90
FT Probable Fe(2+)-trafficking protein.
FT /FTid=PRO 0000246101.
SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;

Query Match 79.6%; Score 387; DB 1; Length 90;
Best Local Similarity 78.2%; Pred. No. 1e-31;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60
Db 1 MARTVFCGYLKQEAEGDLDFQLYPGELGKRIYDNISKEAWGEWMKKQTMVLVNEKLNMMNA 60

QY 61 EHRKLLQEQMVNLFEGKEVHIEGYTP 87
Db 61 EHRKLLQEQMVNLFEGKDVHIEGYVP 87
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Search completed: June 27, 2007, 11:10:39
Job time : 349 secs

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 27, 2007, 11:10:57 ; Search time 50 Seconds
(without alignments)
159.306 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQRAEGQDFQ.....NLFPEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-3859
6	76	15.6	548	2	US-09-167-299-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	2	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
13	67.5	13.9	546	2	US-09-551-974A-2
14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
16	67.5	13.9	546	2	US-09-874-923-2
17	67.5	13.9	546	2	US-08-798-841-2
18	67.5	13.9	982	2	US-09-551-974A-95
19	67.5	13.9	982	2	US-09-565-501A-95
20	67.5	13.9	982	2	US-09-639-206A-95
21	67.5	13.9	982	2	US-09-874-923-95
22	67.5	13.9	1427	2	US-09-551-974A-97
23	67.5	13.9	1427	2	US-09-565-501A-97
24	67.5	13.9	1427	2	US-09-639-206A-97
25	67.5	13.9	1427	2	US-09-874-923-97
26	67.5	13.9	1641	2	US-09-551-974A-96

27	67.5	13.9	1641	2	US-09-565-501A-96	Sequence 96, Appl
28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	395	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5836	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998E-37	Sequence 37, Appl
35	64	13.2	448	2	US-09-270-767-42959	Sequence 42959, A
36	64	13.2	534	2	US-09-312-762A-5	Sequence 5, Appli
37	63.5	13.1	591	2	US-09-370-368-8	Sequence 8, Appli
38	63	13.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
39	63	13.0	569	2	US-09-107-532A-6689	Sequence 6689, Ap
40	62.5	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-18911	Sequence 18911, A
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
43	62	12.8	959	2	US-09-543-681A-6879	Sequence 6879, Ap
44	62	12.8	1394	2	US-09-248-796A-19555	Sequence 19555, A
45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 124, App
48	61.5	12.7	116	2	US-09-562-737-125	Sequence 125, App
49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 26397, A
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 7295, Ap
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 4, Appli
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1, Appli
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 1, Appli
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 1004, Ap
55	61	12.6	444	2	US-09-861-451A-16	Sequence 16, Appl
56	61	12.6	480	2	US-09-438-185A-934	Sequence 934, App
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 4802, Ap
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 4800, Ap
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 6012, Ap
60	60.5	12.4	276	2	US-09-949-016-11703	Sequence 11703, A
61	60.5	12.4	404	2	US-09-914-098-48	Sequence 48, Appl
62	60.5	12.4	640	2	US-09-873-404-2	Sequence 2, Appli
63	60.5	12.4	640	2	US-10-243-735-2	Sequence 2, Appli
64	60.5	12.4	640	2	US-10-730-010-2	Sequence 2, Appli
65	60.5	12.4	1076	2	US-09-171-991-7	Sequence 7, Appli
66	60	12.3	98	2	US-09-270-767-41085	Sequence 41085, A
67	60	12.3	98	2	US-09-270-767-56301	Sequence 56301, A
68	60	12.3	184	2	US-09-270-767-61671	Sequence 61671, A
69	60	12.3	271	2	US-09-248-796A-19265	Sequence 19265, A
70	60	12.3	279	2	US-09-198-452A-221	Sequence 221, App
71	60	12.3	279	2	US-09-438-185A-205	Sequence 205, App
72	60	12.3	331	2	US-09-328-352-6400	Sequence 6400, Ap
73	60	12.3	337	2	US-09-270-767-41746	Sequence 41746, A
74	60	12.3	389	2	US-09-270-767-46116	Sequence 46116, A
75	60	12.3	410	2	US-09-949-016-8705	Sequence 8705, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962


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; Sequence 3, Application US/09167299
; Patent No. 6245539
; GENERAL INFORMATION:
; APPLICANT: Kron, Micheal
; APPLICANT: Hartlein, Micheal
; APPLICANT: Michito, Hirikata
; TITLE OF INVENTION: Human Asparagin
; FILE REFERENCE: Aparaginyl-trRNA Syste
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Brugia malayi
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P10723
; DATABASE ENTRY DATE: 1997-11-01
; US-09-167-299-3

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	Query Match	15.6%;	Score 76;	DB 2;	Length 548;
	Best Local Similarity	30.7%;	Pred. No. 0.77;		
	Matches 27; Conservative	16;	Mismatches 31;	Indels 14;	Gaps 4;
Qy	3	RTIFCTFLQRAEGQDFQLYPGELGKRIYNEISKEAWAQ-WQH-KQTMLINEKKLNMNNA	60		
		:: : :: :: : :: :	: :		
Dd	23	RTLYQAMITKSSKGDFLIRTKDKGQIWEAASKTALKSKWKHYEQEMLKNEKVA-----	77		
Qy	61	EHRKLLEQMVF-----LFEGKEVHIE	83		
		:: :::	::		
Dd	78	--AKMLEKDATEGVKAAALEEAACKVQIE	103		

RESULT 7
US-09-252-991A-24473
; Sequence 24473, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24473
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24473

RESULT 8
US-10-164-595-24
; Sequence 24, Application US/10164595
; Patent No. 6657054

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; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: 1U 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-24

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	Query Match	14.5%;	Score 70.5;	DB 2;	Length 1214;
	Best Local Similarity	28.4%;	Pred. No. 11;		
	Matches 23; Conservative	10;	Mismatches 29;	Indels 19;	Gaps 2;
QY	30 IYNEISKEAWA-----	---QWQHKTMLINEKKLMMNAEHRKLLQEQMVF	73		
	:	:: :	:	: :	::
Dd	944 IYNDSLKNTGSTIAEIRRLRIEIEKLQWLHQQLSEMKHNLELTMAEMRQSLEQRDL	1003			
QY	74 LFEKG---EVHIEGYTPEDKK	91			
	: : :	: :			
Dd	1004 IAEVKKQLELEKQQAAVDETKK	1024			

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RESULT 9
US-09-325-932A-66
; Sequence 66, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Pinus radiata
; US-09-325-932A-66

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RESULT 10
US-08-533-669A-2
; Sequence 2, Application US/08533669A
; Patent No. 5834592
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: LEISHMANIA A
; TITLE OF INVENTION: THERAPY AND I
; NUMBER OF SEQUENCES: 18


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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Leishmania major
US-09-874-923-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
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Db 301 MTRNALCLQRQRKYEA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 342

QY 61 EHRKLEQEMVNFLEFEGKEVHIEG--YTPEDK 90
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Db 343 EHOKAVEEAYIDPEI-AKQKDEGNQYFKEDK 373

RESULT 17
US-08-798-841-2
; Sequence 2, Application US/08798841
; Patent No. 6709661
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,841
; FILING DATE: 12-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-841-2

Query Match      13.9%; Score 67.5; DB 2; Length 546;
Best Local Similarity 28.3%; Pred. No. 8.9;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 MTRNALCLQRQRKYEA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 342

QY 61 EHRKLEQEMVNFLEFEGKEVHIEG--YTPEDK 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 EHOKAVEEAYIDPEI-AKQKDEGNQYFKEDK 373
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RESULT 18
US-09-551-974A-95
; Sequence 95, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-95

Query Match      13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 509 MTRNALCLQRQRKYEA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550

QY 61 EHRKLEQEMVNFLEFEGKEVHIEG--YTPEDK 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 551 EHOKAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 19
US-09-565-501A-95
; Sequence 95, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-95

Query Match      13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;
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QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLLLEQEMVNFLFEGKEVHIEG--YTPEDK 90
Db 551 EHQAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 20
US-09-639-206A-95
; Sequence 95, Application US/09639206A
; Patent No. 6613337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-95

Query Match 13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLLLEQEMVNFLFEGKEVHIEG--YTPEDK 90
Db 551 EHQAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 21
US-09-874-923-95
; Sequence 95, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95

; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-95

Query Match 13.9%; Score 67.5; DB 2; Length 982;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLLLEQEMVNFLFEGKEVHIEG--YTPEDK 90
Db 551 EHQAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 22
US-09-551-974A-97
; Sequence 97, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-97

Query Match 13.9%; Score 67.5; DB 2; Length 1427;
Best Local Similarity 28.3%; Pred. No. 32;
Matches 26; Conservative 12; Mismatches 33; Indels 21; Gaps 5;

QY 1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA 60
Db 509 MTRNALCLQRQKYEAA-IDLY-----KRALVEWRNPDTL-----KKLTECEK 550
QY 61 EHRKLLLEQEMVNFLFEGKEVHIEG--YTPEDK 90
Db 551 EHQAVEEAYIDPEI-AKQKDEGNQYFKEDK 581

RESULT 23
US-09-565-501A-97
; Sequence 97, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 27, 2007, 11:23:07 ; Search time 187 Seconds
(without alignments)
225.415 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	486	100.0	91	3	US-09-955-502-13
4	469	96.5	91	3	US-09-955-502-14
5	469	96.5	91	3	US-09-955-502-16
6	469	96.5	91	3	US-09-955-502-17
7	455	93.6	91	3	US-09-955-502-18
8	453	93.2	88	3	US-09-955-502-15
9	402	82.7	90	3	US-09-955-502-10
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-19
12	388	79.8	91	3	US-09-955-502-5
13	387	79.6	87	3	US-09-955-502-7
14	379	78.0	87	3	US-09-955-502-6
15	373	76.7	87	3	US-09-955-502-8
16	332	68.3	88	3	US-09-955-502-9
17	265	54.5	76	3	US-09-955-502-21
18	255	52.5	87	3	US-09-955-502-2
19	255	52.5	87	3	US-09-955-502-3
20	241	49.6	86	3	US-09-955-502-4
21	231	47.5	87	3	US-09-955-502-25
22	227	46.7	88	3	US-09-955-502-33
23	227	46.7	90	3	US-09-955-502-23
24	226	46.5	89	3	US-09-955-502-22
25	225	46.3	87	3	US-09-955-502-24
26	213	43.8	88	3	US-09-955-502-26
27	213	43.8	88	3	US-09-955-502-27

28	213	43.8	88	3	US-09-955-502-28	Sequence 28, Appl
29	213	43.8	88	5	US-10-467-657-968	Sequence 968, Appl
30	206	42.4	87	3	US-09-955-502-29	Sequence 29, Appl
31	206	42.4	87	3	US-09-955-502-30	Sequence 30, Appl
32	200	41.2	87	3	US-09-955-502-31	Sequence 31, Appl
33	200	41.2	87	3	US-09-955-502-32	Sequence 32, Appl
34	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
35	81	16.7	507	4	US-10-282-122A-68134	Sequence 68134, A
36	78	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
37	74.5	15.3	632	4	US-10-369-493-18744	Sequence 18744, A
38	74.5	15.3	683	6	US-11-087-099-2028	Sequence 2028, Ap
39	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, App
40	71	14.6	311	5	US-10-506-454-862	Sequence 862, App
41	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
42	70.5	14.5	764	5	US-10-491-467-15	Sequence 15, Appl
43	70.5	14.5	786	5	US-10-732-923-4885	Sequence 4885, Ap
44	70.5	14.5	1206	4	US-10-085-198-144	Sequence 144, App
45	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
46	69.5	14.3	481	3	US-09-934-455-466	Sequence 466, App
47	69.5	14.3	481	4	US-10-225-066A-180	Sequence 180, App
48	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
49	69.5	14.3	481	4	US-10-374-780A-396	Sequence 396, App
50	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, App
51	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643,
52	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
53	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166,
54	69	14.2	258	4	US-10-415-478A-36	Sequence 36, Appl
55	69	14.2	258	5	US-10-472-928-2088	Sequence 2088, Ap
56	68.5	14.1	184	4	US-10-393-840-52	Sequence 52, Appl
57	68	14.0	102	3	US-09-864-408A-768	Sequence 768, Appl
58	67.5	13.9	184	4	US-10-219-220-66	Sequence 66, Appl
59	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, App
60	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
61	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appli
62	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appli
63	67.5	13.9	546	4	US-10-098-732A-71	Sequence 71, Appl
64	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, App
65	67.5	13.9	955	3	US-09-991-496-127	Sequence 127, App
66	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
67	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
68	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
69	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
70	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
71	67.5	13.9	1641	3	US-09-991-496-96	Sequence 96, Appl
72	67	13.8	384	6	US-11-188-298-16266	Sequence 16266, A
73	66.5	13.7	190	6	US-11-096-568A-6155	Sequence 6155, Ap
74	66.5	13.7	221	6	US-11-096-568A-6154	Sequence 6154, Ap
75	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A

ALIGNMENTS

RESULT 1
US-09-955-502-11
; Sequence 11, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655

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US-09-955-502-11
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Best Local Similarity 100.0%; Pred. No. 7.9e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRTIFCTFLQREAEAGDQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

RESULT 2
US-09-955-502-12
; Sequence 12, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7EDL933
US-09-955-502-12

Query Match      100.0%; Score 486; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.9e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

RESULT 3
US-09-955-502-13
; Sequence 13, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli O157:H7
US-09-955-502-13

Query Match      100.0%; Score 486; DB 3; Length 91;
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Best Local Similarity 100.0%; Pred. No. 7.9e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAEAGDQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60
Db 1 MSRTIFCTFLQREAEAGDQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91

RESULT 4
US-09-955-502-14
; Sequence 14, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi
US-09-955-502-14

Query Match      96.5%; Score 469; DB 3; Length 91;
Best Local Similarity 94.5%; Pred. No. 6.5e-45;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRTIFCTFLQREAEAGDQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSVLFEGKDVHIEGYTPEDKK 91

RESULT 5
US-09-955-502-16
; Sequence 16, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella dublin
US-09-955-502-16

Query Match      96.5%; Score 469; DB 3; Length 91;
Best Local Similarity 94.5%; Pred. No. 6.5e-45;
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Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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db 1 MSRTFTCYLORDAEGODFOLYPGELGKRIYNEISKDAWAQWQHQTMLINEKKLNMNNA 60

Qy	1	MSRTFCTFLQREAGDQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKKLNMNA	60
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Dd	1	MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWTKQTMLINEKKLNMMDP	60
Qy	61	EHRKLLEQEMWNFLFEGKEVHIEGYTPEDK	90

Db 61 EHRKLEQEMVNFLEFEGKEVHIEGYTPPAK 90

RESULT 10

US-09-955-502-20

; Sequence 20, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; TITLE OF INVENTION: Oxygen-Labile Proteins

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Yersinia pestis

US-09-955-502-20

Query Match 81.5%; Score 396; DB 3; Length 90;

Best Local Similarity 82.2%; Pred. No. 1.1e-36;

Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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Db 1 MSRTIFCTFLKDAERQDFQLYPGELGKRIYNEISKEAWSQWITKQTMLINEKKLSMNI 60

QY 61 EHRKLEQEMVNFLEFEGKEVHIEGYTPEDK 90

Db 61 EDRKLEQEMVNFLEFEGQDVHIAGYTPPSK 90

RESULT 11

US-09-955-502-19

; Sequence 19, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; TITLE OF INVENTION: Oxygen-Labile Proteins

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-955-502-19

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Best Local Similarity 94.9%; Pred. No. 1.2e-36;

Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVNFLEFGK 78

Db 61 EHRKLEQEMVQFLFEGK 78

RESULT 12

US-09-955-502-5

; Sequence 5, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; TITLE OF INVENTION: Oxygen-Labile Proteins

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Actinobacillus actinomycetemcomitans

US-09-955-502-5

Query Match 79.8%; Score 388; DB 3; Length 91;

Best Local Similarity 76.9%; Pred. No. 8.7e-36;

Matches 70; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

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Db 61 EHRKLEQEMVNFLEFEGKDVHIEGYTPPEAK 91

RESULT 13

US-09-955-502-7

; Sequence 7, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; TITLE OF INVENTION: Oxygen-Labile Proteins

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Haemophilus influenzae

US-09-955-502-7

Query Match 79.6%; Score 387; DB 3; Length 87;

Best Local Similarity 78.2%; Pred. No. 1.1e-35;

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QY 61 EHRKLEQEMVNFLEFEGKEVHIEGYTP 87

Db 61 EHRKLEQEMVNFLEFEGKDVHIEGYVP 87

RESULT 14

US-09-955-502-6

; Sequence 6, Application US/09955502

GenCore version 6.2.1
Copyright (c) 1993 - 2007 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 27, 2007, 11:26:12 ; Search time 141 Seconds
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Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAEQDFQ.....NFLPEGKEVHIEGYTPEDKK 91
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1408788 seqs, 343594471 residues
Total number of hits satisfying chosen parameters: 1408788
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB_pep.*
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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB_pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB_pep.*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB_pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	231	47.5 122 6	US-10-419-128-23355 Sequence 23355, A
2	131	27.0 110 6	US-10-603-108-2859 Sequence 2859, Ap
3	85.5	17.6 514 7	US-11-516-230-44315 Sequence 44315, A
4	81	16.7 507 7	US-11-516-230-44283 Sequence 44283, A
5	81	16.7 508 7	US-11-516-230-44299 Sequence 44299, A
6	78	16.0 507 7	US-11-516-230-44263 Sequence 44263, A
7	78	16.0 546 7	US-11-516-230-44265 Sequence 44265, A
8	75.5	15.5 507 7	US-11-516-230-44271 Sequence 44271, A
9	75	15.4 309 6	US-10-526-324-706 Sequence 706, App
10	72	14.8 474 6	US-10-419-128-24473 Sequence 24473, A
11	72	14.8 507 7	US-11-516-230-44261 Sequence 44261, A
12	71.5	14.7 118 6	US-10-703-032-11890 Sequence 11890, A
13	71.5	14.7 566 6	US-10-276-817B-12931 Sequence 12931, A
14	70.5	14.5 285 6	US-10-917-503-11063 Sequence 11063, A
15	70.5	14.5 313 7	US-11-443-428A-890387 Sequence 890387, A
16	70.5	14.5 313 7	US-11-443-428A-890388 Sequence 890388, A
17	70.5	14.5 614 6	US-10-567-867-1402 Sequence 1402, Ap
18	70.5	14.5 647 7	US-11-443-428A-890383 Sequence 890383, A
19	70.5	14.5 702 6	US-10-405-027-3329 Sequence 3329, Ap
20	70.5	14.5 764 7	US-11-582-861-6676 Sequence 6676, Ap
21	70.5	14.5 995 7	US-11-582-861-6675 Sequence 6675, Ap
22	70.5	14.5 1072 7	US-11-443-428A-890379 Sequence 890379, A
23	70.5	14.5 1072 7	US-11-443-428A-890395 Sequence 890395, A
24	70.5	14.5 1107 7	US-11-443-428A-890399 Sequence 890399, A
25	70.5	14.5 1115 7	US-11-443-428A-890396 Sequence 890396, A

26	70.5	14.5	1125	7	US-11-443-428A-890402	Sequence 890402, A
27	70.5	14.5	1135	7	US-11-443-428A-890378	Sequence 890378, A
28	70.5	14.5	1135	7	US-11-443-428A-890392	Sequence 890392, A
29	70.5	14.5	1140	7	US-11-443-428A-890382	Sequence 890382, A
30	70.5	14.5	1140	7	US-11-443-428A-890394	Sequence 890394, A
31	70.5	14.5	1142	7	US-11-443-428A-890386	Sequence 890386, A
32	70.5	14.5	1143	7	US-11-443-428A-890390	Sequence 890390, A
33	70.5	14.5	1159	7	US-11-443-428A-890381	Sequence 890381, A
34	70.5	14.5	1160	7	US-11-443-428A-890393	Sequence 890393, A
35	70.5	14.5	1170	7	US-11-443-428A-890398	Sequence 890398, A
36	70.5	14.5	1180	7	US-11-582-861-6674	Sequence 6674, Ap
37	70.5	14.5	1186	7	US-11-443-428A-890384	Sequence 890384, A
38	70.5	14.5	1186	7	US-11-582-861-6672	Sequence 6672, Ap
39	70.5	14.5	1188	7	US-11-443-428A-890397	Sequence 890397, A
40	70.5	14.5	1188	7	US-11-582-861-6673	Sequence 6673, Ap
41	70.5	14.5	1196	7	US-11-443-428A-890380	Sequence 890380, A
42	69.5	14.3	276	7	US-11-443-428A-861003	Sequence 861003, A
43	69.5	14.3	374	7	US-11-443-428A-861008	Sequence 861008, A
44	69.5	14.3	395	7	US-11-443-428A-861006	Sequence 861006, A
45	69.5	14.3	456	7	US-11-443-428A-861004	Sequence 861004, A
46	69.5	14.3	481	6	US-10-374-780A-396	Sequence 396, App
47	69.5	14.3	481	7	US-11-375-241-64	Sequence 64, Appl
48	69.5	14.3	488	6	US-10-917-503-15108	Sequence 15108, A
49	69.5	14.3	488	7	US-11-371-354-74169	Sequence 74169, A
50	69.5	14.3	488	7	US-11-443-428A-861002	Sequence 861002, A
51	69.5	14.3	488	7	US-11-443-428A-861012	Sequence 861012, A
52	69.5	14.3	498	7	US-11-443-428A-861005	Sequence 861005, A
53	69.5	14.3	507	7	US-11-516-230-44365	Sequence 44365, A
54	69.5	14.3	511	7	US-11-443-428A-861009	Sequence 861009, A
55	69.5	14.3	529	7	US-11-443-428A-861010	Sequence 861010, A
56	69.5	14.3	619	6	US-10-953-349-11813	Sequence 11813, A
57	69.5	14.3	714	6	US-10-953-349-11812	Sequence 11812, A
58	69.5	14.3	750	6	US-10-953-349-11811	Sequence 11811, A
59	68.5	14.1	175	7	US-11-486-448-69349	Sequence 69349, A
60	68.5	14.1	509	7	US-11-516-230-44341	Sequence 44341, A
61	68.5	14.1	514	7	US-11-516-230-44257	Sequence 44257, A
62	68.5	14.1	514	7	US-11-516-230-44381	Sequence 44381, A
63	68	14.0	164	7	US-11-443-428A-919650	Sequence 919650, A
64	68	14.0	213	6	US-10-467-478-806	Sequence 806, App
65	68	14.0	473	6	US-10-474-894-15	Sequence 15, Appl
66	68	14.0	473	6	US-10-760-320A-2528	Sequence 2528, Ap
67	68	14.0	473	7	US-11-582-861-7080	Sequence 7080, Ap
68	68	14.0	2951	6	US-10-467-478-814	Sequence 814, App
69	68	14.0	4560	6	US-10-467-478-551	Sequence 551, App
70	67.5	13.9	1131	7	US-11-330-403-983	Sequence 983, App
71	67.5	13.9	1131	7	US-11-330-403-984	Sequence 984, App
72	67	13.8	79	7	US-11-443-428A-965050	Sequence 965050, A
73	67	13.8	447	6	US-10-219-051B-1778	Sequence 1778, Ap
74	67	13.8	447	6	US-10-743-643-2143	Sequence 2143, Ap
75	67	13.8	447	7	US-11-388-595-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-419-128-23355
; Sequence 23355, Application US/10419128
; Publication No. US20070020624A1
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/10/419,128
; CURRENT FILING DATE: 2003-04-21
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-419-128-23355

Query Match          47.5%; Score 231; DB 6; Length 122;
Best Local Similarity 51.7%; Pred. No. 3.4e-16;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTICTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKKLNMMNA 60
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Db 33 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKADEWQKHQTMLINERRLNMMNA 92

QY 61 EHRKLEQEMVNFLEFEGKEVHIEGYTP 87
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 93 EDRKFLQEQMDKFLSGEDYAKADGYVP 119

RESULT 2
US-10-603-108-2859
; Sequence 2859, Application US/10603108
; Publication No. US20070010665A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-14
; CURRENT APPLICATION NUMBER: US/10/603,108
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 09/540,263
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 60/125,416
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-10-603-108-2859

Query Match          27.0%; Score 131; DB 6; Length 110;
Best Local Similarity 34.9%; Pred. No. 7e-06;
Matches 29; Conservative 13; Mismatches 41; Indels 0; Gaps 0;

QY 5 ICTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKKLNMMNAEHRK 64
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Db 25 VFCKRYQQNLPKLPNPPFPNAKQOEIQDTISAKAWNAWLELQTMLINEKHLMSIDPOAKK 84

QY 65 LLEQEMVNFLEFEGKEVHIEGYTP 87
| : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 85 YLNEQREKFLDNGDYEKPAYKP 107

RESULT 3
US-11-516-230-44315
; Sequence 44315, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
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; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44315
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Desulfotalea psychrophila Lsv54
US-11-516-230-44315

Query Match          17.6%; Score 85.5; DB 7; Length 514;
Best Local Similarity 38.8%; Pred. No. 2.2;
Matches 19; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 18 DFQLYPGELGKRIY-NEISKEAWAQWQHQTMLINEKKLNMMNAEHRKL 65
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 DISLAAGDKVKRVHLNNTKEEIAITWQTGETLLNGKILTGRDAHKRI 362

RESULT 4
US-11-516-230-44283
; Sequence 44283, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; PRIOR FILING DATE: 2006-02-23
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44283
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Pseudomonas putida KT2440
US-11-516-230-44283

Query Match      16.7%; Score 81; DB 7; Length 507;
Best Local Similarity 28.2%; Pred. No. 6.3;
Matches 22; Conservative 16; Mismatches 28; Indels 12; Gaps 3;

QY 13 EAEGQDFQLYP-----GELGKRI-YNEISKEAWAQWQHKTMTLINEKKLNMMNAEHRKL 65
Db 294 ELEAPSLDAYPEIVWEAGPSARRVNLDDITPEEVASWKPGETILLNGKMLTGRDAHAKR- 352
QY 66 LEQEMVNFLFEGKEVHIE 83
Db 353 ----MVEMLNRRGEELPVD 366

RESULT 5
US-11-516-230-44299
; Sequence 44299, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44299
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Chromobacterium violaceum ATCC 12472
US-11-516-230-44299

Query Match      16.7%; Score 81; DB 7; Length 508;
Best Local Similarity 30.2%; Pred. No. 6.3;
Matches 19; Conservative 17; Mismatches 21; Indels 6; Gaps 2;

QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMTLINEKKLNMMNAEHRKLLEQEMVNFLFEGKEV 80
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Db 311 YDASSGKRVLDKITKEEVASWQPGDVLLNGKILTGRDAHAKR-----MIDMLNKGEKL 365
QY 81 HIE 83
Db 366 PVD 368

RESULT 6
US-11-516-230-44263
; Sequence 44263, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Puzio, Piotr
; APPLICANT: Blau, Astrid
; APPLICANT: Herold, Manfred
; APPLICANT: Wendel, Birgit
; APPLICANT: Kamlage, Beate
; APPLICANT: Schauwecker, Florian
; APPLICANT: Looser, Ralf
; TITLE OF INVENTION: Process for the production of fine chemicals
; FILE REFERENCE: 13195-00014-US
; CURRENT APPLICATION NUMBER: US/11/516,230
; CURRENT FILING DATE: 2006-09-06
; PRIOR APPLICATION NUMBER: EP 06110426.1
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110579.7
; PRIOR FILING DATE: 2006-02-28
; PRIOR APPLICATION NUMBER: EP 06110425.3
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110423.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110418.8
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110383.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110378.4
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110367.7
; PRIOR FILING DATE: 2006-02-24
; PRIOR APPLICATION NUMBER: EP 06110327.1
; PRIOR FILING DATE: 2006-02-23
; PRIOR APPLICATION NUMBER: EP 06110325.5
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 73449
; SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
; SEQ ID NO 44263
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Neisseria meningitidis MC58
US-11-516-230-44263

Query Match      16.0%; Score 78; DB 7; Length 507;
Best Local Similarity 30.2%; Pred. No. 13;
Matches 19; Conservative 18; Mismatches 20; Indels 6; Gaps 2;

QY 22 YPGELGKRI-YNEISKEAWAQWQHKTMTLINEKKLNMMNAEHRKLLEQEMVNFLFEGKEV 80
Db 311 YSPDNGKRVLDKITKEEVASWKTGVDVLLNGKILTGRDAHAKRL-----VDMLNKGEEL 365
QY 81 HIE 83
Db 366 PVD 368

RESULT 7
US-11-516-230-44265
; Sequence 44265, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
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OTHER INFORMATION: n is a o r c o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (786944)..(786946)
OTHER INFORMATION: n is a o r c o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (839139)..(839139)
OTHER INFORMATION: n is a o r c o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1128488)..(1128488)
OTHER INFORMATION: n is a o r c o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1128499)..(1128499)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (1128517)..(1128518)
OTHER INFORMATION: n is a o r c o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1128539)..(1128540)
OTHER INFORMATION: n is a o r c o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a o r c o r g o r t.
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NAME/KEY: misc feature
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OTHER INFORMATION: n is a o r c o r g o r t.
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NAME/KEY: misc feature
LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a o r c o r g o r t.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a o r c o r g o r t.
US-10-526-324-706

Query Match 15.4%; Score 75; DB 6; Length 309;
Best Local Similarity 30.0%; Pred. No. 15;
Matches 24; Conservative 13; Mismatches 29; Indels 14; Gaps 2;
Qy 15 EGQDFQLYPGE-----LGKRIYNEISKEAWAQWQHKTMLINE-----KKLNMMNA 60
Db 111 EKTDRVLLIGEGAVKFARLILGFEEYDPITEERLKQWEELRKKLIEKGETKHWKKLNELIK 170
Qy 61 EHRKLEQEMVNFLEFEGKEV 80
Db 171 EYPEVLRSTVGAVAFDGEV 190

RESULT 10
US-10-419-128-24473
Sequence 24473, Application US/10419128
Publication No. US20070020624A1
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/10/419,128
PRIORITY FILING DATE: 2003-04-21
PRIORITY APPLICATION NUMBER: US/09/252,991
PRIORITY FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24473
LENGTH: 474
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-419-128-24473

Query Match 14.8%; Score 72; DB 6; Length 474;
Best Local Similarity 25.6%; Pred. No. 50;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;
Qy 13 EAEGQDFQLYP-----GELGKRI-YNEISKEAWAQWQHKTMLINEKKLNMMNAEHRKL 65
Db 299 ELEAPSLDAYPEIVWEAGPSARRVDLKITPEEVQSWKPGETLLNGKMLTGRDAHAKR- 357
Qy 66 LEQEMVNFLEFEGKEVHIE 83
Db 358 ----MVDMLNKGETLPVD 371

RESULT 11
US-11-516-230-44261
Sequence 44261, Application US/11516230
Publication No. US20070118916A1
GENERAL INFORMATION:
APPLICANT: Plesch, Gunnar
APPLICANT: Puzio, Piotr
APPLICANT: Blau, Astrid
APPLICANT: Herold, Manfred
APPLICANT: Wendel, Birgit
APPLICANT: Kamlage, Beate
APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110579.7
PRIOR FILING DATE: 2006-02-28
PRIOR APPLICATION NUMBER: EP 06110425.3
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110423.8
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110418.8
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110378.4
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110367.7
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110327.1
PRIOR FILING DATE: 2006-02-23
PRIOR APPLICATION NUMBER: EP 06110325.5
PRIOR FILING DATE: 2006-02-23
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax PatentTool according to PatentIN 3.1 format
SEQ ID NO 44261
LENGTH: 507
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa PAO1
US-11-516-230-44261

Query Match 14.8%; Score 72; DB 7; Length 507;
Best Local Similarity 25.6%; Pred. No. 54;
Matches 20; Conservative 18; Mismatches 28; Indels 12; Gaps 3;

Db 43 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLTLTMAEMRQSLQERDRL 102

QY 74 LFEKG---EVHIEGYTPEDKK 91

Db 103 IAEVKKQLELEKQQAQVDETKK 123

RESULT 15

US-11-443-428A-890387

; Sequence 890387, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 890387

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-890387

Query Match 14.5%; Score 70.5; DB 7; Length 313;

Best Local Similarity 28.4%; Pred. No. 44;

Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMMNAEHRKLLLEQEMVNF 73

Db 43 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLTLTMAEMRQSLQERDRL 102

QY 74 LFEKG---EVHIEGYTPEDKK 91

Db 103 IAEVKKQLELEKQQAQVDETKK 123

RESULT 16

US-11-443-428A-890388

; Sequence 890388, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 890388

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-890388

Query Match 14.5%; Score 70.5; DB 7; Length 313;

Best Local Similarity 28.4%; Pred. No. 44;

Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMMNAEHRKLLLEQEMVNF 73

Db 43 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLTLTMAEMRQSLQERDRL 102

QY 74 LFEKG---EVHIEGYTPEDKK 91

Db 103 IAEVKKQLELEKQQAQVDETKK 123

RESULT 17

US-10-567-867-1402

; Sequence 1402, Application US/10567867

; Publication No. US20070105114A1

; GENERAL INFORMATION:

; APPLICANT: Li, Martha

; APPLICANT: Rupnow, Brent A.

; APPLICANT: Webster, Kevin R.

; APPLICANT: Jackson, Donald

; APPLICANT: Wong, Tai W.

; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION

; FILE REFERENCE: D0310 PCT

; CURRENT APPLICATION NUMBER: US/10/567,867

; CURRENT FILING DATE: 2006-01-27

; PRIOR APPLICATION NUMBER: US 60/490,890

; PRIOR FILING DATE: 2003-07-29

; NUMBER OF SEQ ID NOS: 2786

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1402

; LENGTH: 614

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-567-867-1402

Query Match 14.5%; Score 70.5; DB 6; Length 614;

Best Local Similarity 28.4%; Pred. No. 97;

Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMMNAEHRKLLLEQEMVNF 73

Db 372 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLTLTMAEMRQSLQERDRL 431

QY 74 LFEKG---EVHIEGYTPEDKK 91

Db 432 IAEVKKQLELEKQQAQVDETKK 452

RESULT 18

US-11-443-428A-890383

; Sequence 890383, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31


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; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890383
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890383

Query Match      14.5%; Score 70.5; DB 7; Length 647;
Best Local Similarity 28.4%; Pred. No. 1e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMNNAEHRKLLLEQEMVNF 73
    |||::||
Db 405 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLERDRL 464
    |||::||

QY 74 LFEKG---EVHIEGYTPEDKK 91
    :|||::|
Db 465 IAEVKKQLELEKQQAQVDETKK 485
    :|||::|

RESULT 19
US-10-405-027-3329
; Sequence 3329, Application US/10405027
; Publication No. US20070015271A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: FS806PI
; CURRENT APPLICATION NUMBER: US/10/405,027
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 60/369,608
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/376,175
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 5810
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3329
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any amino acid
US-10-405-027-3329

Query Match      14.5%; Score 70.5; DB 6; Length 702;
Best Local Similarity 28.4%; Pred. No. 1.1e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMNNAEHRKLLLEQEMVNF 73
    |||::||
Db 432 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLERDRL 491
    |||::||

QY 74 LFEKG---EVHIEGYTPEDKK 91
    :|||::|
Db 492 IAEVKKQLELEKQQAQVDETKK 512
    :|||::|

RESULT 20
US-11-582-861-6676
; Sequence 6676, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: US 60/728,044
; OTHER INFORMATION: Xaa equals any amino acid
US-11-582-861-6676

Query Match      14.5%; Score 70.5; DB 7; Length 647;
Best Local Similarity 28.4%; Pred. No. 1e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMNNAEHRKLLLEQEMVNF 73
    |||::||
Db 405 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLERDRL 464
    |||::||

QY 74 LFEKG---EVHIEGYTPEDKK 91
    :|||::|
Db 465 IAEVKKQLELEKQQAQVDETKK 485
    :|||::|

RESULT 21
US-11-582-861-6675
; Sequence 6675, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: US 60/728,044
; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6675
; LENGTH: 995
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-6675

Query Match      14.5%; Score 70.5; DB 7; Length 995;
Best Local Similarity 28.4%; Pred. No. 1.7e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

QY 30 IYNEISKEAWA-----QWQHKQTMLINEKKLNMNNAEHRKLLLEQEMVNF 73
    |||::||
Db 753 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLERDRL 812
    |||::||

QY 74 LFEKG---EVHIEGYTPEDKK 91
    :|||::|
Db 813 IAEVKKQLELEKQQAQVDETKK 833
    :|||::|

RESULT 22
US-11-443-428A-890379
; Sequence 890379, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
```

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; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890379
; LENGTH: 1072
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890379

Query Match          14.5%; Score 70.5; DB 7; Length 1072;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

Qy 30 IYNEISKEAWA-----QWQHKTMLINEKKNMNAEHRKLLSEQMVNF 73
    |||:|:|
Db 830 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLEQERDRL 889
    |||:|:|

Qy 74 LFEKG---EVHIEGYTPEDKK 91
    :|:|:|
Db 890 IAEVKKQLELEKQQAQVDETKK 910

RESULT 23
US-11-443-428A-890395
; Sequence 890395, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890395
; LENGTH: 1072
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890395

Query Match          14.5%; Score 70.5; DB 7; Length 1072;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

Qy 30 IYNEISKEAWA-----QWQHKTMLINEKKNMNAEHRKLLSEQMVNF 73
    |||:|:|
Db 830 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLEQERDRL 889
    |||:|:|

Qy 74 LFEKG---EVHIEGYTPEDKK 91
    :|:|:|
Db 890 IAEVKKQLELEKQQAQVDETKK 910

RESULT 24
US-11-443-428A-890399
; Sequence 890399, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
```

```
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890399
; LENGTH: 1107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890399

Query Match          14.5%; Score 70.5; DB 7; Length 1107;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

Qy 30 IYNEISKEAWA-----QWQHKTMLINEKKNMNAEHRKLLSEQMVNF 73
    |||:|:|
Db 837 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLEQERDRL 896
    |||:|:|

Qy 74 LFEKG---EVHIEGYTPEDKK 91
    :|:|:|
Db 897 IAEVKKQLELEKQQAQVDETKK 917

RESULT 25
US-11-443-428A-890396
; Sequence 890396, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 890396
; LENGTH: 1115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-890396

Query Match          14.5%; Score 70.5; DB 7; Length 1115;
Best Local Similarity 28.4%; Pred. No. 1.9e+02;
Matches 23; Conservative 10; Mismatches 29; Indels 19; Gaps 2;

Qy 30 IYNEISKEAWA-----QWQHKTMLINEKKNMNAEHRKLLSEQMVNF 73
    |||:|:|
Db 873 IYNDLSKNTTGSTIAEIRRLRIEIEKQLWLHQQLSEMKHNLELTMAEMRQSLEQERDRL 932
    |||:|:|

Qy 74 LFEKG---EVHIEGYTPEDKK 91
    :|:|:|
Db 933 IAEVKKQLELEKQQAQVDETKK 953
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